PENDING CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

1. (Previously presented) A method of normalizing genetic data for n loci, wherein n is an integer greater than one, comprising

   (a) obtaining genetic data comprising n sets of first and second signal values related in a coordinate system, wherein said first and second signal values are indicative of the levels of a first and second allele, respectively, at n loci;
   (b) identifying a set of sweep points in said coordinate system;
   (c) identifying a set of control points, said control points comprising at least a subset of said signal values that are proximal to said sweep points;
   (d) projecting said control points to a line or curve passing through said sweep points, thereby forming set points;
   (e) determining parameters of a registration transformation equation based on said set of control points_and said set points; and
   (f) transforming said n sets of first and second signal values according to said registration transformation equation and said parameters, thereby normalizing said genetic data.

2. (Original) The method of claim 1, wherein said genetic data is represented in a graphical format.

3. (Original) The method of claim 2, wherein said graphical format comprises Cartesian coordinates.

4. (Original) The method of claim 1, wherein said genetic data is provided in a tabular format.

5. (Cancelled).

6. (Original) The method of claim 1, wherein said identifying sweep points comprises

(i) identifying an upper limit on a line or curve through said coordinate system; and

(ii) locating said sweep points between the origin of each axis and said upper limit.

7. (Original) The method of claim 6, wherein said upper limit has a value in a first dimension that is greater than or equal to the first dimension of any of said signal values.

8. (Original) The method of claim 6, further comprising a step of identifying a lower limit on said line or curve, and wherein said locating comprises locating said sweep points between said lower limit and said upper limit.

9. (Original) The method of claim 1, wherein said identifying a set of control points comprises triangulation using pairs of signal values and a sweep point.

10. (Original) The method of claim 9, wherein said triangulation comprises Delaunay triangulation.

11. (Original) The method of claim 1, wherein said identifying a set of control points comprises computing all pair-wise distances between the signal values and each sweep point.

12. (Cancelled)

13. (Previously presented) The method of claim 1, wherein said registration transformation equation comprises affine transformation projecting said control points onto said set points.

14. (Previously presented) The method of claim 1, wherein said registration transformation equation comprises linear conformational transformation projecting said control points onto said set points.

15. (Previously presented) The method of claim 1, wherein said registration transformation equation comprises projective transformation projecting said control points onto said set points.

16. (Previously presented) The method of claim 1, wherein said registration transformation equation comprises polynomial transformation projecting said control points onto said set points.

17. (Original) The method of claim 1, wherein said determining parameters of a registration transformation equation comprises global registration.

18. (Original) The method of claim 1, wherein said set of control points is fewer in number compared to the number of first and second signal values.

19. (Original) The method of claim 1, wherein said sweep points are located on a line or curve through said coordinate system when represented graphically.

20. (Original) The method of claim 19, wherein said line comprises an axis of said coordinate system.

21. (Original) The method of claim 1, wherein said sweep points are spaced along said line or curve in a manner selected from the group consisting of linear, log-linear and non-linear.

22. (Original) The method of claim 1, wherein said coordinate system comprises two dimensions.

23. (Original) The method of claim 22, wherein step (b) comprises identifying two sets of sweep points in said coordinate system; and step (c) comprises identifying two sets of control points.

24. (Original) The method of claim 1, wherein said genetic data comprises n sets of first, second and third signal values related in a coordinate system, wherein said first, second and third signal values are indicative of the levels of a first, second and third allele, respectively, at n loci.

25. (Original) The method of claim 24, wherein said coordinate system comprises three dimensions.

26. (Original) The method of claim 24, wherein step (b) comprises identifying three sets of sweep points in said coordinate system; and step (c) comprises identifying three sets of control points.

27. (Original) The method of claim 1, wherein said registration transformation is selected from the group consisting of rotation of said n sets of first and second signal values, translation of said n sets of first and second signal values, scaling of said n sets of first and second signal values, and sheer of said n sets of first and second signal values.

28. (Previously presented) The method of claim 1, further comprising a step of balancing said n sets of first and second signal values by a balancing signal transformation, thereby balancing the probability function for the distribution of said n sets of first and second signal values as a function of signal intensity.

29. (Previously presented) The method of claim 1, wherein said balancing signal transformation is selected from the group consisting of natural logarithm, base 2 logarithm, base 10 logarithm, arctangent, square root, nth root, wherein $n > 2$, and Box-Cox.

30-46 (Cancelled)

47. (Currently amended) A [genotyping] system for analysis of genetic data, comprising

(a) an array reader configured to detect signals from separate locations on an array substrate;

(b) a computer processor configured to receive signal values from said array reader;

(c) a normalization module comprising commands for

(i) reading said signal values;

(ii) identifying a set of sweep points for said signal values in a coordinate system;

(iii) identifying a set of control points, said control points comprising at least a subset of said signal values that are proximal to said sweep points;

(iv) projecting said control points to a line or curve passing through said sweep points, thereby forming set points;

(v) determining parameters of a registration transformation equation based on said control points and said set points; and

(d) (vi) genotyping module comprising commands for

(i) reading said normalized genetic data;

(ii) comparing fit of said normalized genetic data to each of a plurality of cluster models using an artificial neural network, thereby determining a best fit cluster model; and

(iii) assigning said signal values to at least one cluster according to said best fit cluster model, wherein if said best fit cluster model contains at least one actual cluster and at least one missing cluster, then using a second artificial neural network to propose a location for said at least one missing cluster.

48. (Currently amended) A method of determining the alleles present at n loci for an individual [a genotype score], comprising

(a) obtaining genetic data comprising n sets of first and second signal values related in a coordinate system, wherein said first and second signal values are indicative of the levels of a first and second allele, respectively, at n loci;

(b) identifying a set of sweep points in said coordinate system;

(c) identifying a set of control points, said control points comprising at least a subset of said signal values that are proximal to said sweep points;

(d) projecting said control points to a line or curve passing through said sweep points, thereby forming set points;

(e) determining parameters of a registration transformation equation based on said set of control points and said set points; and

(f) transforming said n sets of first and second signal values according to said registration transformation equation and said parameters, thereby normalizing said genetic data;

(g) comparing fit of said normalized genetic data to each of a plurality of cluster models using an artificial neural network, thereby determining a best fit cluster model;

(h) assigning said signal values to at least one cluster according to said best fit cluster model, wherein if said best fit cluster model contains at least one actual cluster and at least one missing cluster, then using a second artificial neural network to propose a location for said at least one missing cluster; and

(i) determining, for an individual, the alleles present at said n loci.

49. (Previously presented) The system of claim 47, wherein said commands for identifying sweep points comprise commands for

(i) identifying an upper limit on a line or curve through said coordinate system; and

(ii) locating said sweep points between the origin of each axis and said upper limit.

50. (Previously presented) The system of claim 49, wherein said normalization module further comprises commands for identifying a lower limit on said line or curve, and wherein said locating comprises locating said sweep points between said lower limit and said upper limit.

51. (Previously presented) The system of claim 47, wherein said identifying a set of control points comprises triangulation using pairs of signal values and a sweep point.

52. (Previously presented) The system of claim 51, wherein said triangulation comprises Delaunay triangulation.

53. (Previously presented) The system of claim 47, wherein said identifying a set of control points comprises computing all pair-wise distances between the signal values and each sweep point.

54. (Previously presented) The system of claim 47, wherein said registration transformation equation comprises affine transformation projecting said control points onto said set points.

55. (Previously presented) The system of claim 47, wherein said registration transformation equation comprises linear conformational transformation projecting said control points onto said set points.

56. (Previously presented) The system of claim 47, wherein said registration transformation equation comprises projective transformation projecting said control points onto said set points.

57. (Previously presented) The system of claim 47, wherein said registration transformation equation comprises polynomial transformation projecting said control points onto said set points.

58. (Previously presented) The system of claim 47, wherein said determining parameters of a registration transformation equation comprises global registration.

59. (Previously presented) The system of claim 47, wherein said sweep points are located on a line or curve through said coordinate system when represented graphically.

60. (Previously presented) The system of claim 59, wherein said line comprises an axis of said coordinate system.

61. (Previously presented) The system of claim 47, wherein said sweep points are spaced along said line or curve in a manner selected from the group consisting of linear, log-linear and non-linear.

62. (Previously presented) The system of claim 47, wherein said coordinate system comprises two dimensions.

63. (Previously presented) The system of claim 47, wherein said coordinate system comprises three dimensions.

64. (Previously presented) The method of claim 48, wherein said genetic data is represented in a graphical format.

65. (Previously presented) The method of claim 64, wherein said graphical format comprises Cartesian coordinates.

66. (Previously presented) The method of claim 48, wherein said genetic data is provided in a tabular format.

67. (Previously presented) The method of claim 48, wherein said identifying sweep points comprises

(i) identifying an upper limit on a line or curve through said coordinate system; and

(ii) locating said sweep points between the origin of each axis and said upper limit.

68. (Previously presented) The method of claim 67, wherein said upper limit has a value in a first dimension that is greater than or equal to the first dimension of any of said signal values.

69. (Previously presented) The method of claim 67, further comprising a step of identifying a lower limit on said line or curve, and wherein said locating comprises locating said sweep points between said lower limit and said upper limit.

70. (Previously presented) The method of claim 48, wherein said identifying a set of control points comprises triangulation using pairs of signal values and a sweep point.

71. (Previously presented) The method of claim 70, wherein said triangulation comprises Delaunay triangulation.

72. (Previously presented) The method of claim 48, wherein said identifying a set of control points comprises computing all pair-wise distances between the signal values and each sweep point.

73. (Previously presented) The method of claim 48, wherein said registration transformation equation comprises affine transformation projecting said control points onto said set points.

74. (Previously presented) The method of claim 48, wherein said registration transformation equation comprises linear conformational transformation projecting said control points onto said set points.

75. (Previously presented) The method of claim 48, wherein said registration transformation equation comprises projective transformation projecting said control points onto said set points.

76. (Previously presented) The method of claim 48, wherein said registration transformation equation comprises polynomial transformation projecting said control points onto said set points.

77. (Previously presented) The method of claim 48, wherein said determining parameters of a registration transformation equation comprises global registration.

78. (Previously presented) The method of claim 48, wherein said set of control points is fewer in number compared to the number of first and second signal values.

79. (Previously presented) The method of claim 48, wherein said sweep points are located on a line or curve through said coordinate system when represented graphically.

80. (Previously presented) The method of claim 79, wherein said line comprises an axis of said coordinate system.

81. (Previously presented) The method of claim 48, wherein said sweep points are spaced along said line or curve in a manner selected from the group consisting of linear, log-linear and non-linear.

82. (Previously presented) The method of claim 48, wherein said coordinate system comprises two dimensions.

83. (Previously presented) The method of claim 82, wherein step (b) comprises identifying two sets of sweep points in said coordinate system; and step (c) comprises identifying two sets of control points.

84. (Previously presented) The method of claim 48, wherein said genetic data comprises n sets of first, second and third signal values related in a coordinate system, wherein said first, second and third signal values are indicative of the levels of a first, second and third allele, respectively, at n loci.

85. (Previously presented) The method of claim 84, wherein said coordinate system comprises three dimensions.

86. (Previously presented) The method of claim 84, wherein step (b) comprises identifying three sets of sweep points in said coordinate system; and step (c) comprises identifying three sets of control points.

87. (Previously presented) The method of claim 48, wherein said registration transformation is selected from the group consisting of rotation of said n sets of first and second signal values, translation of said n sets of first and second signal values, scaling of said n sets of first and second signal values, and sheer of said n sets of first and second signal values.

88. (Previously presented) The method of claim 48, further comprising a step of balancing said n sets of first and second signal values by a signal transformation, thereby balancing the probability function for the distribution of said n sets of first and second signal values as a function of signal intensity.

89. (Previously presented) The method of claim 48, wherein said signal transformation is selected from the group consisting of natural logarithm, base 2 logarithm, base 10 logarithm, arctangent, square root, nth root, wherein $n > 2$, and Box-Cox.

90. (New) The method of claim 1, wherein step (a) comprises obtaining genetic data comprising n sets of first and second signal values for n loci related in a coordinate system, wherein said first signal value is indicative of the level of a first allele at a locus of said n loci and said second signal value is indicative of the level of a second allele at said locus.

91. (New) The method of claim 48, wherein step (a) comprises obtaining genetic data comprising n sets of first and second signal values for n loci related in a coordinate system, wherein said first signal value is indicative of the level of a first allele at a locus of said n loci and said second signal value is indicative of the level of a second allele at said locus.